

SEQUENCE LISTING



<110> McCarthy, Sean A.

<120> NOVEL HUMAN DICKKOPF-RELATED PROTEIN AND NUCLEIC ACID
MOLECULES AND USES THEREFOR

<130> MNI-108CP2

<140> 09/263,022

<141> 1999-03-05

<150> 08/843,704

<151> 1997-04-16

<150> 08/842,898

<151> 1997-04-17

<150> 60/071,589

<151> 1998-01-15

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<170> PatentIn Ver. 2.0

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<223> 'n' at position 1146 may be any nucleotide

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ccc gct ccg acg gcg acc tcg gct cca gtc aag ccc ggc ccg gct ctc 151
Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu
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Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Ala Ser Ser Glu Val Asn	
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ctg gca aac tta cct ccc agc tat cac aat gag acc aac aca gac acg	343
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aac gtt gga aat aat acc atc cat gtg cac cga gaa att cac aag ata	391
Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile	
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 Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
 50 55 60
 Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
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 Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
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 Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
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 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
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 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
 225 230 235 240
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Val	Pro	Thr	Ala	Pro	Ala	Pro	Ala	Pro	Thr	Ala	Thr	Ser	Ala	Pro	Val	
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Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu	
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Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu	
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ctg cat ggg gcc cgg aag ggc tca cag tgc ctg tct gac acg gac tgc 265
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Cys Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp
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65 70 75 80
Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp Ala
85 90 95
Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala
100 105 110
Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys
115 120 125
Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser
130 135 140
Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His
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Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys
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Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr Leu Asn Ser
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Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro Leu Gly Gly
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gct gcg ggg cac cca ggc tct gca gtc agc gcc gcg ccg gga atc ctg 309
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Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr Gln Pro Tyr
70 75 80
ccg tgc gca gag gac gag gag tgc ggc act gat gag tac tgc gct agt 405
Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr Cys Ala Ser
85 90 95
ccc acc cgc gga ggc gac gca ggc gtg caa atc tgt ctc gcc tgc agg 453
Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu Ala Cys Arg
100 105 110 115
aag cgc cga aaa cgc tgc atg cgt cac gct atg tgc tgc ccc ggc aat 501
Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys Pro Gly Asn
120 125 130
tac tgc aaa aat gga ata tgt gtg tct tct gat caa aat cat ttc cga 549
Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn His Phe Arg
135 140 145
gga gaa att gag gaa acc atc act gaa agc ttt ggt aat gat cat agc 597
Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His Ser
150 155 160
acc ttg gat ggc tat tcc aga aga acc acc ttg tct tca aaa atg tat 645
Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser Lys Met Tyr
165 170 175

cac acc aaa gga caa gaa ggt tct gtt tgt ctc cgg tca tca gac tgt 693
His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys
180 185 190 195

gcc tca gga ttg tgt tgt gct aga cac ttc tgg tcc aag atc tgt aaa 741
Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys Ile Cys Lys
200 205 210

cct gtc ctg aaa gaa ggt caa gtg tgt acc aag cat agg aga aaa ggc 789
Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg Arg Lys Gly
215 220 225

tct cat gga cta gaa ata ttc cag cgt tgt tac tgt gga gaa ggt ctg 837
Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly Glu Gly Leu
230 235 240

tct tgc cgg ata cag aaa gat cac cat caa gcc agt aat tct tct agg 885
Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn Ser Ser Arg
245 250 255

ctt cac act tgt cag aga cac taaaccagct atccaaatgc agtgaactcc 936
Leu His Thr Cys Gln Arg His
260 265

ttttatataa tagatgctat gaaaaccttt tatgaccttc atcaactcaa tcctaaggat 996

atacaagttc tgtggtttca gttaagcatt ccaataacac cttccaaaaa cctggagtgt 1056

aagagctttg tttctttatg gaactccoct gtgattgcag taaattactg tattgtaaat 1116

tctcagtgtg gcacttacct gtaaattgcaa tgaaactttt aattattttt ctaaagggtgc 1176

tgcaactgcct atttttcttc ttgttatgta aatttttgta cacattgatt gttatcttga 1236

ctgacaaata ttctatattg aactgaagta aatcatttca gcttatagtt cttaaaagca 1296

taacccttta ccccatthta ttctagagtc tagaacgcaa ggatctcttg gaatgacaaa 1356

tgataggtac ctaaaatgta acatgaaaat actagcttat tttctgaaat gtactatctt 1416

aatgcttaaa ttatatttcc ctttaggctg tgatagtttt tgaaataaaa ttttaacattt 1476

aatatcatga aatgttataa gtagacataa aaaaaaaaaa aaaaaaaaaa gggcgccgc 1536

<210> 8

<211> 266.

<212> PRT

<213> Homo sapiens

<400> 8

Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala Met
1 5 10 15

Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr
20 25 30

Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro
35 40 45

Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro
 50 55 60
 Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr
 65 70 75 80
 Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr
 85 90 95
 Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu
 100 105 110
 Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys
 115 120 125
 Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn
 130 135 140
 His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn
 145 150 155 160
 Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser
 165 170 175
 Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser
 180 185 190
 Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys
 195 200 205
 Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg
 210 215 220
 Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly
 225 230 235 240
 Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn
 245 250 255
 Ser Ser Arg Leu His Thr Cys Gln Arg His
 260 265

<210> 9
 <211> 798
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(798)

<400> 9
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 Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala Met
 1 5 10 15
 gta gcg gcg gct ctc ggc ggc cac cct ctg ctg gga gtg agc gcc acc 96
 Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr
 20 25 30

ttg aac tcg gtt ctc aat tcc aac gct atc aag aac ctg ccc cca ccg	144
Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro	
35 40 45	
ctg ggc ggc gct gcg ggg cac cca ggc tct gca gtc agc gcc gcg ccg	192
Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro	
50 55 60	
gga atc ctg tac ccg ggc ggg aat aag tac cag acc att gac aac tac	240
Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr	
65 70 75 80	
cag ccg tac ccg tgc gca gag gac gag gag tgc ggc act gat gag tac	288
Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr	
85 90 95	
tgc gct agt ccc acc cgc gga ggg gac gca ggc gtg caa atc tgt ctc	336
Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu	
100 105 110	
gcc tgc agg aag cgc cga aaa cgc tgc atg cgt cac gct atg tgc tgc	384
Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys	
115 120 125	
ccc ggg aat tac tgc aaa aat gga ata tgt gtg tct tct gat caa aat	432
Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn	
130 135 140	
cat ttc cga gga gaa att gag gaa acc atc act gaa agc ttt ggt aat	480
His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn	
145 150 155 160	
gat cat agc acc ttg gat ggg tat tcc aga aga acc acc ttg tct tca	528
Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser	
165 170 175	
aaa atg tat cac acc aaa gga caa gaa ggt tct gtt tgt ctc cgg tca	576
Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser	
180 185 190	
tca gac tgt gcc tca gga ttg tgt tgt gct aga cac ttc tgg tcc aag	624
Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys	
195 200 205	
atc tgt aaa cct gtc ctg aaa gaa ggt caa gtg tgt acc aag cat agg	672
Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg	
210 215 220	
aga aaa ggc tct cat gga cta gaa ata ttc cag cgt tgt tac tgt gga	720
Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly	
225 230 235 240	
gaa ggt ctg tct tgc cgg ata cag aaa gat cac cat caa gcc agt aat	768
Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn	
245 250 255	
tct tct agg ctt cac act tgt cag aga cac	798
Ser Ser Arg Leu His Thr Cys Gln Arg His	
260 265	

<210> 10
 <211> 702
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(537)

<400> 10
 gaa ttc ggc acg agg gtt ggg agg tat tgc cac agt ccc cac caa gga 48
 Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
 1 5 10 15

tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga 96
 Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
 20 25 30

gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc 144
 Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
 35 40 45

cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt 192
 Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
 50 55 60

act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg 240
 Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
 65 70 75 80

gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa 288
 Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
 85 90 95

ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg 336
 Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
 100 105 110

ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc 384
 Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
 115 120 125

cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg 432
 His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
 130 135 140

ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa 480
 Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 145 150 155 160

gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt 528
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
 165 170 175

cag aaa att tgatcaccat tgaggaacat catcaattgc agactgtgaa 577
 Gln Lys Ile

gttgtgtatt taatgcatta tagcatggtg gaaaataagg ttcagatgca gaagaatggc 637

taaaataaga aacgtgataa gaatatagat gatcacaaaa aaaaaaaaaa aaaagatgcg 697

gccgc

702

<210> 11
<211> 179
<212> PRT
<213> Homo sapiens

<400> 11
Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
1 5 10 15
Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
20 25 30
Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
35 40 45
Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
50 55 60
Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
65 70 75 80
Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
85 90 95
Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
100 105 110
Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
115 120 125
His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
130 135 140
Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
145 150 155 160
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
165 170 175
Gln Lys Ile

<210> 12
<211> 537
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(537)

<400> 12
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Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
1 5 10 15

tca tgc gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga	96
Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg	
20 25 30	
gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc	144
Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile	
35 40 45	
cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt	192
Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly	
50 55 60	
act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg	240
Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu	
65 70 75 80	
gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa	288
Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys	
85 90 95	
ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg	336
Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly	
100 105 110	
ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc	384
Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu	
115 120 125	
cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg	432
His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly	
130 135 140	
ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa	480
Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys	
145 150 155 160	
gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt	528
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys	
165 170 175	
cag aaa att	537
Gln Lys Ile	

<210> 13
 <211> 928
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (75)..(800)

<400> 13
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 agaaggggagc ggggt atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg 110
 Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg
 1 5 10

aaaaaaaaaa aaaaaaaaaa aaaaaaattg gcggccgc

928

<210> 14
<211> 242
<212> PRT
<213> Homo sapiens

<400> 14
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
1 5 10 15
Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
20 25 30
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
35 40 45
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
50 55 60
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
65 70 75 80
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
85 90 95
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
100 105 110
Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
115 120 125
Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
130 135 140
Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His
145 150 155 160
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
165 170 175
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu
180 185 190
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
195 200 205
His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg
210 215 220
Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg
225 230 235 240
Gln Leu

<210> 15
<211> 726

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(726)

<400> 15

atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg cat ctg ctg gtc	48
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val	
1 5 10 15	
ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc gct gca gct cct	96
Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro	
20 25 30	
atc cat gat gct gac gcc caa gag agc tcc ttg ggt ctc aca ggc ctc	144
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu	
35 40 45	
cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg aaa ggt aac ctg	192
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu	
50 55 60	
ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg gac ttc cgg ggc	240
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly	
65 70 75 80	
ctc cct ggg aac tac cac aaa gag gag aac cag gag cac cag ctg ggg	288
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly	
85 90 95	
aac aac acc ctc tcc agc cac ctc cag atc gac aag atg acc gac aac	336
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn	
100 105 110	
aag aca gga gag gtg ctg atc tcc gag aat gtg gtg gca tcc att caa	384
Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln	
115 120 125	
cca gcg gag ggg agc ttc gag ggt gat ttg aag gta ccc agg atg gag	432
Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu	
130 135 140	
gag aag gag gcc ctg gta ccc atc cag aag gcc acg gac agc ttc cac	480
Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His	
145 150 155 160	
aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att aag ctg cca cgg	528
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg	
165 170 175	
cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac tgg ctc agc gag	576
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu	
180 185 190	
aag cga cac cgc ctg cag gcc atc cgg gat gga ctc cgc aag ggg acc	624
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr	
195 200 205	

cac aag gac gtc cta gaa gag ggg acc gag agc tcc tcc cac tcc agg	672
His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg	
210 215 220	
ctg tcc ccc cga aag acc cac tta ctg tac atc ctc agg ccc tct cgg	720
Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg	
225 230 235 240	
cag ctg	726
Gln Leu	
<210> 16	
<211> 2380	
<212> DNA	
<213> Homo sapiens	
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<222> (109)..(1155)	
<400> 26	
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gctcagcttt gttcattcga attgggcggc ggccagcgcg gaacaaac atg cag cgg	117
Met Gln Arg	
1	
ctc ggg ggt att ttg ctg tgt aca ctg ctg gcg gcg gcg gtc ccc act	165
Leu Gly Gly Ile Leu Leu Cys Thr Leu Leu Ala Ala Ala Val Pro Thr	
5 10 15	
gct cct gct cct tcc ccg acg gtc act tgg act ccg gcg gag ccg ggc	213
Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala Glu Pro Gly	
20 25 30 35	
cca gct ctc aac tac cct cag gag gaa gct acg ctc aat gag atg ttt	261
Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe	
40 45 50	
cga gag gtg gag gag ctg atg gaa gac act cag cac aaa ctg cgc agt	309
Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser	
55 60 65	
gcc gtg gag gag atg gag gcg gaa gaa gca gct gct aaa acg tcc tct	357
Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Lys Thr Ser Ser	
70 75 80	
gag gtg aac ctg gca agc tta cct ccc aac tat cac aat gag acc agc	405
Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn Glu Thr Ser	
85 90 95	
acg gag acc agg gtg gga aat aac aca gtc cat gtg cac cag gaa gtt	453
Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His Gln Glu Val	
100 105 110 115	
cac aag ata acc aac aac cag agt gga cag gtg gtc ttt tct gag aca	501
His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe Ser Glu Thr	
120 125 130	

gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc cat gaa tgt	549
Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser His Glu Cys	
135 140 145	
atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag ttc tcc agc	597
Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln Phe Ser Ser	
150 155 160	
ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg cta tgc acc	645
Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met Leu Cys Thr	
165 170 175	
cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg ggt cac tgc	693
Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp Gly His Cys	
180 185 190 195	
acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt gac aac cag	741
Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys Asp Asn Gln	
200 205 210	
agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga ggc ctg ctg	789
Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu	
215 220 225	
ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc tgc cat gac	837
Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp	
230 235 240	
ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg gag cct gaa	885
Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Glu	
245 250 255	
gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta tgc cag cca	933
Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro	
260 265 270 275	
cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc gtg ggc agc	981
His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe Val Gly Ser	
280 285 290	
cat gac cac agt gag gag agc cag ctg ccc agg gag gcc ccg gat gag	1029
His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala Pro Asp Glu	
295 300 305	
tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag ctg gaa gac	1077
Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu Leu Glu Asp	
310 315 320	
ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg cct gcc cct	1125
Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly Pro Ala Pro	
325 330 335	
gtg gag tca cta ggc gga gag gag gag att taggccaga cccagctgag	1175
Val Glu Ser Leu Gly Glu Glu Glu Ile	
340 345	
tcaactggtag atgtgcaata gaaatggcta atttattttc ccaggagtgt ccccaagtgt	1235
ggaatggccg cagctccttc ccagtagctt ttcctctggc ttgacaaggt acagtgcagt	1295
acattttcttc cagccgccct gcttctctga cttgggaaag acaggcatgg cgggtaaggg	1355

cagcggtagag tcgtccctcg ctgttgctag aaacgctgtc ttgttcttca tggatggaag 1415
 atttgtttga agggagagga tgggaagggg tgaagtctgc tcatgatgga tttgggggat 1475
 acaggagga ggatgcctgc cttgcagacg tggacttggc aaaatgtaac ctttgctttt 1535
 gtcttgcgcc gctcccatgg gctgaggcag tggctacaca agagctatgc tgctctgtgg 1595
 cctcccatat attcatccct gtgtttcagc tcctacctca ctgtcagcac agcccttcat 1655
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 ggtcaggctg acttgcatgt cctctaacg ttctgtacag tgtggtggac actgtcttcc 1895
 accgactgct tcaatacctc tgaaagccag tgctcggagt gcagttcgtg taaattaatt 1955
 tgcaggaagt atacttggct aattgtaggg ctaggattgt gaatgaaatt tgcaaagtcg 2015
 cttagcaaca atggaaagcc tttctcagtc acaccgagaa gtcacaacca agccaggttg 2075
 tgtagagtac agctgtgaca tacagacaga agaaggctgg gctggatgtc aggctcaga 2135
 tgacggtttc aggtgccagg aactattacc attctgtatc tatccagagt tattaataatt 2195
 gaaagttgca cacatttgta taagcatgcc tttctcctga gttttaaatt atatgtatac 2255
 acaaacatgt ggccctcaaa gatcatgcac aaaccactac tctttgctaa ttcttggact 2315
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 gccgc 2380

<210> 17
 <211> 349
 <212> PRT
 <213> Homo sapiens

<400> 17
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 1 5 10 15
 Val Pro Thr Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala
 20 25 30
 Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn
 35 40 45
 Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
 50 55 60
 Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
 65 70 75 80
 Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn
 85 90 95

Glu	Thr	Ser	Thr	Glu	Thr	Arg	Val	Gly	Asn	Asn	Thr	Val	His	Val	His			
			100					105					110					
Gln	Glu	Val	His	Lys	Ile	Thr	Asn	Asn	Gln	Ser	Gly	Gln	Val	Val	Phe			
		115					120					125						
Ser	Glu	Thr	Val	Ile	Thr	Ser	Val	Gly	Asp	Glu	Glu	Gly	Lys	Arg	Ser			
		130				135						140						
His	Glu	Cys	Ile	Ile	Asp	Glu	Asp	Cys	Gly	Pro	Thr	Arg	Tyr	Cys	Gln			
		145			150					155					160			
Phe	Ser	Ser	Phe	Lys	Tyr	Thr	Cys	Gln	Pro	Cys	Arg	Asp	Gln	Gln	Met			
				165					170					175				
Leu	Cys	Thr	Arg	Asp	Ser	Glu	Cys	Cys	Gly	Asp	Gln	Leu	Cys	Ala	Trp			
			180					185					190					
Gly	His	Cys	Thr	Gln	Lys	Ala	Thr	Lys	Gly	Gly	Asn	Gly	Thr	Ile	Cys			
		195					200					205						
Asp	Asn	Gln	Arg	Asp	Cys	Gln	Pro	Gly	Leu	Cys	Cys	Ala	Phe	Gln	Arg			
		210				215					220							
Gly	Leu	Leu	Phe	Pro	Val	Cys	Thr	Pro	Leu	Pro	Val	Glu	Gly	Glu	Leu			
		225			230					235					240			
Cys	His	Asp	Pro	Thr	Ser	Gln	Leu	Leu	Asp	Leu	Ile	Thr	Trp	Glu	Leu			
				245					250					255				
Glu	Pro	Glu	Gly	Ala	Leu	Asp	Arg	Cys	Pro	Cys	Ala	Ser	Gly	Leu	Leu			
			260					265					270					
Cys	Gln	Pro	His	Ser	His	Ser	Leu	Val	Tyr	Met	Cys	Lys	Pro	Ala	Phe			
		275					280					285						
Val	Gly	Ser	His	Asp	His	Ser	Glu	Glu	Ser	Gln	Leu	Pro	Arg	Glu	Ala			
		290				295					300							
Pro	Asp	Glu	Tyr	Glu	Asp	Val	Gly	Phe	Ile	Gly	Glu	Val	Arg	Gln	Glu			
		305			310					315					320			
Leu	Glu	Asp	Leu	Glu	Arg	Ser	Leu	Ala	Gln	Glu	Met	Ala	Phe	Glu	Gly			
				325					330					335				
Pro	Ala	Pro	Val	Glu	Ser	Leu	Gly	Gly	Glu	Glu	Glu	Ile						
			340					345										

<210> 18
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 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1)..(1047)

<400> 18
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Met Gln Arg Leu Gly Gly Ile Leu Leu Cys Thr Leu Leu Ala Ala Ala
1 5 10 15

gtc ccc act gct cct gct cct tcc ccg acg gtc act tgg act ccg gcg 96
Val Pro Thr Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala
20 25 30

gag ccg ggc cca gct ctc aac tac cct cag gag gaa gct acg ctc aat 144
Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45

gag atg ttt cga gag gtg gag gag ctg atg gaa gac act cag cac aaa 192
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60

ctg cgc agt gcc gtg gag gag atg gag gcg gaa gaa gca gct gct aaa 240
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80

acg tcc tct gag gtg aac ctg gca agc tta cct ccc aac tat cac aat 288
Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn
85 90 95

gag acc agc acg gag acc agg gtg gga aat aac aca gtc cat gtg cac 336
Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His
100 105 110

cag gaa gtt cac aag ata acc aac aac cag agt gga cag gtg gtc ttt 384
Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe
115 120 125

tct gag aca gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc 432
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser
130 135 140

cat gaa tgt atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag 480
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln
145 150 155 160

ttc tcc agc ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg 528
Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met
165 170 175

cta tgc acc cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg 576
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp
180 185 190

ggt cac tgc acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt 624
Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys
195 200 205

gac aac cag agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga 672
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220

ggc ctg ctg ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc 720
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240

tgc cat gac ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg	768
Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu	
245 250 255	
gag cct gaa gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta	816
Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu	
260 265 270	
tgc cag cca cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc	864
Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe	
275 280 285	
gtg ggc agc cat gac cac agt gag gag agc cag ctg ccc agg gag gcc	912
Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala	
290 295 300	
ccg gat gag tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag	960
Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu	
305 310 315 320	
ctg gaa gac ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg	1008
Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly	
325 330 335	
cct gcc cct gtg gag tca cta ggc gga gag gag gag att	1047
Pro Ala Pro Val Glu Ser Leu Gly Gly Glu Glu Glu Ile	
340 345	

<210> 19
 <211> 8
 <212> PRT
 <213> synthtic construct

<400> 19
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 20
 <211> 3696
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (712)..(1500)

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 atcgctgcgc tggcagcgat tcgctgtctc ttgtgagtca ggggacaacg cttcgggggca 120
 actgtgagtg cgcgtgtggg ggacctcgat tctcttcaga tctcaggat tcgggtccggg 180
 gacgtctcct gatcccctac taaagcgctt gctaactttg aaaaggagca ctgtgtcctg 240
 caaagtttga cacataaagg ataggaaaag agaggagaga aaagcaactg agttgaagga 300
 gaaggagctg atgcgggcct cctgatcaat taagaggaga gttaaaccgc cgagatccccg 360

gcgggaccaa	ggaggtgcg	ggcaagaagg	aacggaagcg	gtgcgatcca	cagggctggg	420
ttttcttgca	ccttggttca	cgcctccttg	gcgagaaagc	gcctcgcatt	tgattgcttc	480
cagttattgc	agaacttcct	gtcctggtgg	agaagcgggt	ctcgccttgg	ttccgcta	540
ttctgtcctg	aggcgtgaga	ctgagttcat	agggtccttg	gtccccgaac	caggaagggt	600
tgagggaaca	caatctgcaa	gccccgcga	cccaagtgag	gggccccgtg	ttggggtcct	660
ccctcccttt	gcattcccac	ccctccgggc	tttgcgcttt	cctgggggacc	c cct cgc	717
					Pro Arg	
					1	
cgg gag atg gcc gcg ttg atg cgg agc aag gat tcg tcc tgc tgc ctg	765					
Arg Glu Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu						
5 10 15						
ctc cta ctg gcc gcg gtg ctg atg gtg gag agc tca cag atc ggc agt	813					
Leu Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser						
20 25 30						
tcg cgg gcc aaa ctc aac tcc atc aag tcc tct ctg ggc ggg gag acg	861					
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu Thr						
35 40 45 50						
cct ggt cag gcc gcc aat cga tct gcg ggc atg tac caa gga ctg gca	909					
Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly Leu Ala						
55 60 65						
ttc ggc ggc agt aag aag ggc aaa aac ctg ggg cag gcc tac cct tgt	957					
Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala Tyr Pro Cys						
70 75 80						
agc agt gat aag gag tgt gaa gtt ggg agg tat tgc cac agt ccc cac	1005					
Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys His Ser Pro His						
85 90 95						
caa gga tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc	1053					
Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys						
100 105 110						
cac cga gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc	1101					
His Arg Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile						
115 120 125 130						
tgt atc cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg	1149					
Cys Ile Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu						
135 140 145						
gat ggt act cgg cac aga gat cga aac cac ggt cat tac tca aac cat	1197					
Asp Gly Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His						
150 155 160						
gac ttg gga tgg cag aat cta gga aga cca cac act aag atg tca cat	1245					
Asp Leu Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His						
165 170 175						
ata aaa ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att	1293					
Ile Lys Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile						
180 185 190						

gaa ggg ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca	1341
Glu Gly Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro	
195 200 205 210	
gtg ctc cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct	1389
Val Leu His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser	
215 220 225	
cat ggg ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct	1437
His Gly Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser	
230 235 240	
tgc aaa gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat	1485
Cys Lys Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His	
245 250 255	
gtg tgt cag aaa att tgatcacat tgaggaacat catcaattgc agactgtgaa	1540
Val Cys Gln Lys Ile	
260	
gttgtgtatt taatgcatta tagcatggtg gaaaataagg ttcagatgca gaagaatggc	1600
taaaataaga aacgtgataa gaatatagat gatcacaaaa agggagaaaag aaaacatgaa	1660
ctgaatagat tagaatgggt gacaaatgca gtgcagccag tgtttccatt atgcaacttg	1720
tctatgtaaa taatgtacac atttgtggaa aatgctatta ttaagagaac aagcacacag	1780
tggaaattac tgatgagtag catgtgactt tccaagagtt taggttgtgc tggaggagag	1840
gtttccttca gattgctgat tgcttatata aataacctac atgccagatt tctattcaac	1900
gtagaggttt aacaaaatac tctagaata acttggtata caatagggtc taaaaataaa	1960
attgctaaac aagaaatgaa aacatggagc attgttaatt tacaacagaa aattaccttt	2020
tgatttgtaa cactacttct gctgttcaat caagagtctt gtagataag aaaaaaatca	2080
gtcaatatatt ccaaataatt gcaaaataat ggccagttgt ttaggaaggc ctttaggaag	2140
acaaataaat aacaaacaaa cagccacaaa tacttttttt tcaaaatttt agttttacct	2200
gtaattaata agaactgata caagacaaaa acagttcctt cagattctac ggaatgacag	2260
tatatctctc tttatcctat gtgattcctg ctctgaatgc attatatttt ccaaagtata	2320
cccataaatt gtgactagta aaatacttac acagagcaga attttcacag atggcaaaaa	2380
aatttaaaga tgtccaatat atgtgggaaa agagctaaca gagagatcat tatttcttaa	2440
agattggcca taacctgtat ttgatagaa ttagattggt aaatacatgt attcatacat	2500
actctgtggt aatagagact tgagctggat ctgtactgca ctggagtaag caagaaaatt	2560
gggaaaactt tttcgtttgt tcaggttttg gcaacacata gatcatatgt ctgaggcaca	2620
agttggctgt tcattcttga aaccagggga tgcacagtct aaatgaatat ctgcatggga	2680
tttgatcat aatatttact atgcagatga attcagtgtg aggtcctgtg tccgtactat	2740

cctcaaatta tttattttat agtgctgaga tcctcaaata atctcaattt caggaggttt 2800
 cacaaaatgg actcctgaag tagacagagt agtgaggttt cattgccctc tataagcttc 2860
 tgactagcca atggcatcat ccaattttct tcccaaacct ctgcagcatc tgctttattg 2920
 ccaaagggtt agtttcgggtt ttctgcagcc attgcgggtta aaaaatataa gtaggataac 2980
 ttgtaaaacc tgcattattgc taatctatag acaccacagt ttctaaattc tttgaaacca 3040
 ctttactact ttttttaaac ttaactcagt tctaaatact ttgtctggag cacaaaacaa 3100
 taaaagggtta tcttatagtt gtgactttta actttttagt accacaattc actttttagt 3160
 tttcttttac ttaaattcca tctgcagtct caaatttaag ttctcccagt agagattgag 3220
 tttgagcctg tatatctatt aaaaatttca acttcccaca tatatttact aagatgatta 3280
 agacttacat tttctgcaca ggtctgcaaa aacaaaaatt ataaactagt ccatccaaga 3340
 accaaagttt gtataaacag gttgctataa gcttggtgaa atgaaaatgg aacatttcaa 3400
 tcaaacattt cctatataac aattattata tttacaattt gggttctgca atatttttct 3460
 tatgtccacc cttttaaaaa ttattatttg aagtaattta tttacaggaa atgttaatga 3520
 gatgtatttt cttatagaga tatttcttac agaaagcttt gtagcagaat atatttgcag 3580
 ctattgactt tgtaatttag gaaaaatgta taataagata aaatctatta aatttttctc 3640
 ctctaaaaac tgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagggc ggccgc 3696

<210> 21
 <211> 263
 <212> PRT
 <213> Homo sapiens

<400> 21
 Pro Arg Arg Glu Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys
 1 5 10 15
 Cys Leu Leu Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile
 20 25 30
 Gly Ser Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly
 35 40 45
 Glu Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
 50 55 60
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala Tyr
 65 70 75 80
 Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys His Ser
 85 90 95
 Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys
 100 105 110

Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn
115 120 125

Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro
130 135 140

Ala Leu Asp Gly Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser
145 150 155 160

Asn His Asp Leu Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met
165 170 175

Ser His Ile Lys Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp
180 185 190

Cys Ile Glu Gly Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys
195 200 205

Lys Pro Val Leu His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys
210 215 220

Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly
225 230 235 240

Leu Ser Cys Lys Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg
245 250 255

Leu His Val Cys Gln Lys Ile
260

<210> 22
<211> 789
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(789)

<400> 22
cct cgc cgg gag atg gcc gcg ttg atg cgg agc aag gat tcg tcc tgc 48
Pro Arg Arg Glu Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys
1 5 10 15

tgc ctg ctc cta ctg gcc gcg gtg ctg atg gtg gag agc tca cag atc 96
Cys Leu Leu Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile
20 25 30

ggc agt tcg cgg gcc aaa ctc aac tcc atc aag tcc tct ctg ggc ggc 144
Gly Ser Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly
35 40 45

gag acg cct ggt cag gcc gcc aat cga tct gcg ggc atg tac caa gga 192
Glu Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
50 55 60

ctg gca ttc ggc ggc agt aag aag ggc aaa aac ctg ggc cag gcc tac 240
Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala Tyr
65 70 75 80

cct tgt agc agt gat aag gag tgt gaa gtt ggg agg tat tgc cac agt	288
Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys His Ser	
85 90 95	
ccc cac caa gga tca tgc gcc tgc atg gtg tgt cgg aga aaa aag aag	336
Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys	
100 105 110	
cgc tgc cac cga gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat	384
Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn	
115 120 125	
ggc atc tgt atc cca gtt act gaa agc atc tta acc cct cac atc ccg	432
Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro	
130 135 140	
gct ctg gat ggt act cgg cac aga gat cga aac cac ggt cat tac tca	480
Ala Leu Asp Gly Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser	
145 150 155 160	
aac cat gac ttg gga tgg cag aat cta gga aga cca cac act aag atg	528
Asn His Asp Leu Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met	
165 170 175	
tca cat ata aaa ggg cat gaa gga gac ccc tgc cta cga tca tca gac	576
Ser His Ile Lys Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp	
180 185 190	
tgc att gaa ggg ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc	624
Cys Ile Glu Gly Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys	
195 200 205	
aaa cca gtg ctc cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag	672
Lys Pro Val Leu His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys	
210 215 220	
ggg tct cat ggg ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc	720
Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly	
225 230 235 240	
ctg tct tgc aaa gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga	768
Leu Ser Cys Lys Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg	
245 250 255	
ctc cat gtg tgt cag aaa att	789
Leu His Val Cys Gln Lys Ile	
260	

<210> 23

<211> 54

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus sequence

<220>

<223> Xaa's at positions

2, 3, 5, 6, 8-12, 14-26, 28, 29, 31-36, 38-42, 45-48, and

50-53 may be any amino acid

<220>

<223> Xaa's at postions 22-26 may be absent

<400> 23

Cys Xaa Xaa Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa
35 40 45

Cys Xaa Xaa Xaa Xaa Cys
50

<210> 24

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence

<220>

<223> Xaa's at positions
2,5,8,9,11,14-23,25,27-30,32,33,35-53,60,62,63,65,
68,70,71,73-96,98,100,101,104, and 106-122 may be
any amino acid

<220>

<223> Xaa's at positions 22,23,51-58,89-96 and 116-122
may be absent

<400> 24

Cys Xaa Xaa Xaa Xaa Asp Cys Xaa Xaa Gly Xaa Cys Cys Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Pro Xaa Xaa Xaa Xaa Gly Xaa
20 25 30

Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Pro
50 55 60

Xaa Xaa Xaa Xaa Gly Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Cys Xaa Cys Xaa Xaa Gly Leu Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
115 120

<210> 25
<211> 87
<212> PRT
<213> Homo sapiens

<400> 25
Ile Asn Leu Glu Asn Gly Glu Leu Cys Met Asn Ser Ala Gln Cys Lys
1 5 10 15
Ser Asn Cys Cys Gln His Ser Ser Ala Leu Gly Leu Ala Arg Cys Thr
20 25 30
Ser Met Ala Ser Glu Asn Ser Glu Cys Ser Val Lys Thr Leu Tyr Gly
35 40 45
Ile Tyr Tyr Lys Cys Pro Cys Glu Arg Gly Leu Thr Cys Glu Gly Asp
50 55 60
Lys Thr Ile Val Gly Ser Ile Thr Asn Thr Asn Phe Gly Ile Cys His
65 70 75 80
Asp Ala Gly Arg Ser Lys Gln
85

<210> 26
<211> 835
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (57)..(746)

<400> 25
gaattcggca cgaggcagaa ggcgcgaatg aaggcaaagc ctcccaccca cctgca atg 59
Met
1
tgt cga ctg agg gtc ttg ctg ctg ctg ctc ccc ttg gcc ttc gtg tcc 107
Cys Arg Leu Arg Val Leu Leu Leu Leu Leu Pro Leu Ala Phe Val Ser
5 10 15
tcc tct gct ctc ccc atc cat gat gtc gac tct cag cag aac acc tcc 155
Ser Ser Ala Leu Pro Ile His Asp Val Asp Ser Gln Gln Asn Thr Ser
20 25 30
ggg ttc ctg ggc ctt cag agg ctt ctc caa agc ttt agt cga ctg ttc 203
Gly Phe Leu Gly Leu Gln Arg Leu Leu Gln Ser Phe Ser Arg Leu Phe
35 40 45
cta aaa aat gac ctg cta cga gac ctg gac aac ttc ttc tcc tcc ccc 251
Leu Lys Asn Asp Leu Leu Arg Asp Leu Asp Asn Phe Phe Ser Ser Pro
50 55 60 65

atg gac ttc cga gac ctt cct agg aac ttc cat cag gaa gag aac cag 299
Met Asp Phe Arg Asp Leu Pro Arg Asn Phe His Gln Glu Glu Asn Gln
70 75 80

gag cac aga atg ggc aac cat acc ctc tcc agc cac cta cag ata gac 347
Glu His Arg Met Gly Asn His Thr Leu Ser Ser His Leu Gln Ile Asp
85 90 95

aag gtg act gac aac cag aca ggg gag gtg cac atc tcg gag aaa gtc 395
Lys Val Thr Asp Asn Gln Thr Gly Glu Val His Ile Ser Glu Lys Val
100 105 110

gag gcc tcc att gag cca gaa cgg aac ccg gaa ggg gac tgg aag gtt 443
Glu Ala Ser Ile Glu Pro Glu Arg Asn Pro Glu Gly Asp Trp Lys Val
115 120 125

ccc aaa gta gaa gca aaa gag ccc ccg gtg cct gtg cag aag gtc acc 491
Pro Lys Val Glu Ala Lys Glu Pro Pro Val Val Val Gln Lys Val Thr
130 135 140 145

gac agc ttg cac cca gag ccc cgg cag gtg gct ttc tgg atc atg aag 539
Asp Ser Leu His Pro Glu Pro Arg Gln Val Ala Phe Trp Ile Met Lys
150 155 160

atg cca agg cgg agg acc cag ccc gat gtc cag gat gga ggc cgc tgg 587
Met Pro Arg Arg Arg Thr Gln Pro Asp Val Gln Asp Gly Gly Arg Trp
165 170 175

ctc ata gaa aag cga cat cgc atg cag gcc atc cgg gat ggg ctc cgt 635
Leu Ile Glu Lys Arg His Arg Met Gln Ala Ile Arg Asp Gly Leu Arg
180 185 190

gga ggc gcc cgt gag gac agc ctg gag gat ggg gtc cat atc ccc caa 683
Gly Gly Ala Arg Glu Asp Ser Leu Glu Asp Gly Val His Ile Pro Gln
195 200 205

cac gcc aag ctg cct gtc aga aag aca cac ttt ctc tac atc ctc agg 731
His Ala Lys Leu Pro Val Arg Lys Thr His Phe Leu Tyr Ile Leu Arg
210 215 220 225

cca tcc caa cag ctg taagtgggga ccagatgtcc cacaccctac cccaacacca 786
Pro Ser Gln Gln Leu
230

tatggaaata aaggttttct tacatctaaa aaaaaaaaaa aaaaaaaaaa 835

<210> 27

<211> 230

<212> PRT

<213> Mus musculus

<400> 27

Met Cys Arg Leu Arg Val Leu Leu Leu Leu Leu Pro Leu Ala Phe Val
1 5 10 15

Ser Ser Ser Ala Leu Pro Ile His Asp Val Asp Ser Gln Gln Asn Thr
20 25 30

Ser Gly Phe Leu Gly Leu Gln Arg Leu Leu Gln Ser Phe Ser Arg Leu
35 40 45

Phe Leu Lys Asn Asp Leu Leu Arg Asp Leu Asp Asn Phe Phe Ser Ser
50 55 60

Pro Met Asp Phe Arg Asp Leu Pro Arg Asn Phe His Gln Glu Glu Asn
65 70 75 80

Gln Glu His Arg Met Gly Asn His Thr Leu Ser Ser His Leu Gln Ile
85 90 95

Asp Lys Val Thr Asp Asn Gln Thr Gly Glu Val His Ile Ser Glu Lys
100 105 110

Val Glu Ala Ser Ile Glu Pro Glu Arg Asn Pro Glu Gly Asp Trp Lys
115 120 125

Val Pro Lys Val Glu Ala Lys Glu Pro Pro Val Pro Val Gln Lys Val
130 135 140

Thr Asp Ser Leu His Pro Glu Pro Arg Gln Val Ala Phe Trp Ile Met
145 150 155 160

Lys Met Pro Arg Arg Arg Thr Gln Pro Asp Val Gln Asp Gly Gly Arg
165 170 175

Trp Leu Ile Glu Lys Arg His Arg Met Gln Ala Ile Arg Asp Gly Leu
180 185 190

Arg Gly Gly Ala Arg Glu Asp Ser Leu Glu Asp Gly Val His Ile Pro
195 200 205

Gln His Ala Lys Leu Pro Val Arg Lys Thr His Phe Leu Tyr Ile Leu
210 215 220

Arg Pro Ser Gln Gln Leu
225 230

<210> 28
<211> 690
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(690)

<400> 28
atg tgt cga ctg agg gtc ttg ctg ctg ctg ctc ccc ttg gcc ttc gtg 48
Met Cys Arg Leu Arg Val Leu Leu Leu Leu Leu Pro Leu Ala Phe Val
1 5 10 15

tcc tcc tct gct ctc ccc atc cat gat gtc gac tct cag cag aac acc 96
Ser Ser Ser Ala Leu Pro Ile His Asp Val Asp Ser Gln Gln Asn Thr
20 25 30

tcc ggg ttc ctg ggc ctt cag agg ctt ctc caa agc ttt agt cga ctg 144
Ser Gly Phe Leu Gly Leu Gln Arg Leu Leu Gln Ser Phe Ser Arg Leu
35 40 45

ttc cta aaa aat gac ctg cta cga gac ctg gac aac ttc ttc tcc tcc	192
Phe Leu Lys Asn Asp Leu Leu Arg Asp Leu Asp Asn Phe Phe Ser Ser	
50 55 60	
ccc atg gac ttc cga gac ctt cct agg aac ttc cat cag gaa gag aac	240
Pro Met Asp Phe Arg Asp Leu Pro Arg Asn Phe His Gln Glu Glu Asn	
65 70 75 80	
cag gag cac aga atg ggc aac cat acc ctc tcc agc cac cta cag ata	288
Gln Glu His Arg Met Gly Asn His Thr Leu Ser Ser His Leu Gln Ile	
85 90 95	
gac aag gtg act gac aac cag aca ggg gag gtg cac atc tcg gag aaa	336
Asp Lys Val Thr Asp Asn Gln Thr Gly Glu Val His Ile Ser Glu Lys	
100 105 110	
gtc gag gcc tcc att gag cca gaa cgg aac ccg gaa ggg gac tgg aag	384
Val Glu Ala Ser Ile Glu Pro Glu Arg Asn Pro Glu Gly Asp Trp Lys	
115 120 125	
gtt ccc aaa gta gaa gca aaa gag ccc ccg gtg cct gtg cag aag gtc	432
Val Pro Lys Val Glu Ala Lys Glu Pro Pro Val Pro Val Gln Lys Val	
130 135 140	
acc gac agc ttg cac cca gag ccc cgg cag gtg gct ttc tgg atc atg	480
Thr Asp Ser Leu His Pro Glu Pro Arg Gln Val Ala Phe Trp Ile Met	
145 150 155 160	
aag atg cca agg cgg agg acc cag ccc gat gtc cag gat gga ggc cgc	528
Lys Met Pro Arg Arg Arg Thr Gln Pro Asp Val Gln Asp Gly Gly Arg	
165 170 175	
tgg ctc ata gaa aag cga cat cgc atg cag gcc atc cgg gat ggg ctc	576
Trp Leu Ile Glu Lys Arg His Arg Met Gln Ala Ile Arg Asp Gly Leu	
180 185 190	
cgt gga ggc gcc cgt gag gac agc ctg gag gat ggg gtc cat atc ccc	624
Arg Gly Gly Ala Arg Glu Asp Ser Leu Glu Asp Gly Val His Ile Pro	
195 200 205	
caa cac gcc aag ctg cct gtc aga aag aca cac ttt,ctc tac atc ctc	672
Gln His Ala Lys Leu Pro Val Arg Lys Thr His Phe Leu Tyr Ile Leu	
210 215 220	
agg cca tcc caa cag ctg	690
Arg Pro Ser Gln Gln Leu	
225 230	

<210> 29

<211> 51

<212> PRT

<213> Artificial Sequence

<220>

<223> Xaa at positions

3-5,7,9-15,18,20-22,24-27,29,31,33,34,36-39,42,44,
45, and 47-50 may be any amino acid

<220>

<223> Description of Artificial Sequence: consensus
sequence

<400> 29

Leu Pro Xaa Xaa Xaa His Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly
1 5 10 15

Asn Xaa Thr Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Lys Xaa Thr Xaa Asn
20 25 30

Xaa Xaa Gly Xaa Xaa Xaa Xaa Ser Glu Xaa Val Xaa Xaa Ser Xaa Xaa
35 40 45

Xaa Xaa Glu
50

<210> 30

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 30

cagtgagtgc tgtggagacc

20

<210> 31

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 31

tcttcagtca ggctcctctc

20

<210> 32

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 32

acctgcaatg tgctcgactga g

21

<210> 33

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 33
cacttacagc tggttggaatg

20

<210> 34
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<223> Xaa at position 1 may be any amino acid

<400> 34
Xaa Val Leu Asp Phe Asn Asn Ile Arg Ser
1 5 10

<210> 35
<211> 10
<212> PRT
<213> Homo sapiens

<400> 35
Ser Gln Gly Arg Lys Gly Gln Glu Gly Ser
1 5 10

<210> 36
<211> 272
<212> PRT
<213> Mus musculus

<400> 36
Met Met Val Val Cys Ala Pro Ala Ala Val Arg Phe Leu Ala Val Phe
1 5 10 15
Thr Met Met Ala Leu Cys Ser Leu Pro Leu Leu Gly Ala Ser Ala Thr
20 25 30
Leu Asn Ser Val Leu Ile Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro
35 40 45
Pro Leu Gly Gly Ala Gly Gly Gln Pro Gly Ser Ala Val Ser Val Ala
50 55 60
Pro Gly Val Leu Tyr Glu Gly Gly Asn Lys Tyr Gln Thr Leu Asp Asn
65 70 75 80
Tyr Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Ser Asp Glu
85 90 95
Tyr Cys Ser Ser Pro Ser Arg Gly Ala Ala Gly Val Gly Gly Val Gln
100 105 110
Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Thr His Ala
115 120 125
Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Met Pro Ser
130 135 140

Asp	His	Ser	His	Phe	Pro	Arg	Gly	Glu	Ile	Glu	Glu	Ser	Ile	Ile	Glu
145					150					155					160
Asn	Leu	Gly	Asn	Asp	His	Asn	Ala	Ala	Ala	Gly	Asp	Gly	Tyr	Pro	Arg
			165						170					175	
Arg	Thr	Thr	Leu	Thr	Ser	Lys	Ile	Tyr	His	Thr	Lys	Gly	Gln	Glu	Gly
			180					185					190		
Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ala	Ala	Gly	Leu	Cys	Cys	Ala
		195					200					205			
Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln
	210					215					220				
Val	Cys	Thr	Lys	His	Lys	Arg	Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe
225					230					235					240
Gln	Arg	Cys	Tyr	Cys	Gly	Glu	Gly	Leu	Ala	Cys	Arg	Ile	Gln	Lys	Asp
				245					250					255	
His	His	Gln	Ala	Ser	Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His
			260					265					270		

<210> 37
 <211> 259
 <212> PRT
 <213> *Xenopus laevis*

<400> 37

Met	Gly	Ser	Asn	Met	Phe	Pro	Val	Pro	Leu	Ile	Val	Phe	Trp	Gly	Phe
1				5					10					15	
Ile	Leu	Asp	Gly	Ala	Leu	Gly	Phe	Val	Met	Met	Thr	Asn	Ser	Asn	Ser
			20					25					30		
Ile	Lys	Asn	Val	Pro	Ala	Ala	Pro	Ala	Gly	Gln	Pro	Ile	Gly	Tyr	Tyr
		35					40					45			
Pro	Val	Ser	Val	Ser	Pro	Asp	Ser	Leu	Tyr	Asp	Ile	Ala	Asn	Lys	Tyr
	50					55					60				
Gln	Pro	Leu	Asp	Ala	Tyr	Pro	Leu	Tyr	Ser	Cys	Thr	Glu	Asp	Asp	Asp
65					70					75					80
Cys	Ala	Leu	Asp	Glu	Phe	Cys	His	Ser	Ser	Arg	Asn	Gly	Asn	Ser	Leu
				85					90					95	
Val	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	Cys	Leu	Arg	Asp	Ala
			100					105					110		
Met	Cys	Cys	Thr	Gly	Asn	Tyr	Cys	Ser	Asn	Gly	Ile	Cys	Val	Pro	Val
		115					120					125			
Glu	Gln	Asp	Gln	Glu	Arg	Phe	Gln	His	Gln	Gly	Tyr	Leu	Glu	Glu	Thr
	130					135					140				
Ile	Leu	Glu	Asn	Tyr	Asn	Asn	Ala	Asp	His	Ala	Thr	Met	Asp	Thr	His
145					150					155					160

Ser Lys Leu Thr Thr Ser Pro Ser Gly Met Gln Pro Phe Lys Gly Arg
165 170 175
Asp Gly Asp Val Cys Leu Arg Ser Thr Asp Cys Ala Pro Gly Leu Cys
180 185 190
Cys Ala Arg His Phe Trp Ser Lys Ile Cys Lys Pro Val Leu Asp Glu
195 200 205
Gly Gln Val Cys Thr Lys His Arg Arg Lys Gly Ser His Gly Leu Glu
210 215 220
Ile Phe Gln Arg Cys His Cys Gly Ala Gly Leu Ser Cys Arg Leu Gln
225 230 235 240
Lys Gly Glu Phe Thr Thr Val Pro Lys Thr Ser Arg Leu His Thr Cys
245 250 255
Gln Arg His

<210> 38
<211> 350
<212> PRT
<213> Gallus gallus

<400> 38
Met Arg Arg Gly Glu Gly Pro Ala Pro Arg Arg Arg Trp Leu Leu Leu
1 5 10 15
Leu Ala Val Leu Ala Ala Leu Cys Cys Ala Ala Ala Gly Ser Gly Gly
20 25 30
Arg Arg Arg Ala Ala Ser Leu Gly Glu Met Leu Arg Glu Val Glu Ala
35 40 45
Leu Met Glu Asp Thr Gln His Lys Leu Arg Asn Ala Val Gln Glu Met
50 55 60
Glu Ala Glu Glu Glu Gly Ala Lys Lys Leu Ser Glu Val Asn Phe Glu
65 70 75 80
Asn Leu Pro Pro Thr Tyr His Asn Glu Ser Asn Thr Glu Thr Arg Ile
85 90 95
Gly Asn Lys Thr Val Gln Thr His Gln Glu Ile Asp Lys Val Thr Asp
100 105 110
Asn Arg Thr Gly Ser Thr Ile Phe Ser Glu Thr Ile Ile Thr Ser Ile
115 120 125
Lys Gly Gly Glu Asn Lys Arg Asn His Glu Cys Ile Ile Asp Glu Asp
130 135 140
Cys Glu Thr Gly Lys Tyr Cys Gln Phe Ser Thr Phe Glu Tyr Lys Cys
145 150 155 160
Gln Pro Cys Lys Thr Gln His Thr His Cys Ser Arg Asp Val Glu Cys
165 170 175

Cys	Gly	Asp	Gln	Leu	Cys	Val	Trp	Gly	Glu	Cys	Arg	Lys	Ala	Thr	Ser	180	185	190
Arg	Gly	Glu	Asn	Gly	Thr	Ile	Cys	Glu	Asn	Gln	His	Asp	Cys	Asn	Pro	195	200	205
Gly	Thr	Cys	Cys	Ala	Phe	Gln	Lys	Glu	Leu	Leu	Phe	Pro	Val	Cys	Thr	210	215	220
Pro	Leu	Pro	Glu	Glu	Gly	Glu	Pro	Cys	His	Asp	Pro	Ser	Asn	Arg	Leu	225	230	235
Leu	Asn	Leu	Ile	Thr	Trp	Glu	Leu	Glu	Pro	Asp	Gly	Val	Leu	Glu	Arg	245	250	255
Cys	Pro	Cys	Ala	Ser	Gly	Leu	Ile	Cys	Gln	Pro	Gln	Ser	Ser	His	Ser	260	265	270
Thr	Thr	Ser	Val	Cys	Glu	Leu	Ser	Ser	Asn	Glu	Thr	Arg	Lys	Asn	Glu	275	280	285
Lys	Glu	Asp	Pro	Leu	Asn	Met	Asp	Glu	Met	Pro	Phe	Ile	Ser	Leu	Ile	290	295	300
Pro	Arg	Asp	Ile	Leu	Ser	Asp	Tyr	Glu	Glu	Ser	Ser	Val	Ile	Gln	Glu	305	310	315
Val	Arg	Lys	Glu	Leu	Glu	Ser	Leu	Glu	Asp	Gln	Ala	Gly	Val	Lys	Ser	325	330	335
Glu	His	Asp	Pro	Ala	His	Asp	Leu	Phe	Leu	Gly	Asp	Glu	Ile			340	345	350

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Cont